

# SEQUENCE LISTING

<110> Glaxo Group Limited  
Knick, Vincent C  
Stimmel, Julie B  
Thurmond, Linda M

<120> Antibody combination

<130> PU3513

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<170> PatentIn Ver. 2.1

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<211> 740

<212> DNA

<213> Artificial Sequence

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<221> CDS

<222> (24)..(740)

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<223> Description of Artificial Sequence: Synthetic  
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Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Val Met Thr Gln Ser  
15 20 25

cca ctc tcc ctg ccc gtc acc cct gga gag ccg gcc tcc atc tcc tgt 149  
Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys  
30 35 40

agg tct agt aag aat ctc ctg cat agt aat ggc atc act tat ttg tat 197  
Arg Ser Ser Lys Asn Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr  
45 50 55

tgg tac ctg cag aag cca ggg cag tct cca cag ctc ctg atc tat cag 245  
Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln  
60 65 70

atg tcc aac ctt gcc tca ggg gtc cct gac agg ttc agt agc agt gga 293  
Met Ser Asn Leu Ala Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly  
75 80 85 90

tca ggc aca gat ttt aca ctg aaa atc agc aga gtg gag gct gag gat 341  
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp

95										100					105					
gtt	ggg	gtt	tat	tac	tgt	gct	caa	aat	cta	gag	att	cct	cgg	acg	ttc	389				
Val	Gly	Val	Tyr	Tyr	Cys	Ala	Gln	Asn	Leu	Glu	Ile	Pro	Arg	Thr	Phe					
			110					115					120							
ggc	caa	ggg	acc	aag	gtg	gag	atc	aaa	cgt	acg	gtg	gct	gca	cca	tct	437				
Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser					
		125					130					135								
gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	485				
Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala					
	140					145					150									
tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	533				
Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val					
155					160					165					170					
cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	581				
Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser					
				175				180					185							
gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	629				
Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr					
			190					195					200							
ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	677				
Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys					
		205					210					215								
gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	725				
Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn					
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Arg	Gly	Glu	Cys																	
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 sequence

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 Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn Leu  
 35 40 45  
 Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro  
 50 55 60

Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Leu	Ala	Ser	65	70	75	80
Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	85	90	95	
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	100	105	110	
Ala	Gln	Asn	Leu	Glu	Ile	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	115	120	125	
Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	130	135	140	
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	145	150	155	160
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	165	170	175	
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	180	185	190	
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	195	200	205	
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	210	215	220	
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	225	230	235			

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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 gaggtgttag gtgctgtcct tgctgtcctg ctctgtgaca ctctcctggg agttaccoga 180  
 ttggagggcg ttatccacct tccactgtac ttggcctct ctgggataga agttattcag 240  
 caggcacaca acagaggcag ttccagattt caactgctca tcagatggcg ggaagatgaa 300  
 gacagatggt gcagccaccg tacgtttgat ctccaccttg gtcccttggc cgaacgtccg 360  
 aggaatctct agattttgag cacagtaata aacccaaca tcctcagcct ccaactctgct 420  
 gattttcagt gtaaaatctg tgcctgatcc actgctactg aacctgtcag ggaccctga 480  
 ggcaagggtg gacatctgat agatcaggag ctgtggagac tgccctggct tctgcaggta 540  
 ccaatacaaa taagtgatgc cattactatg caggagattc ttactagacc tacaggagat 600  
 ggaggccggc totccagggg tgacggggcag ggagagtga gactgagtca tcacaatatc 660  
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<222> (24)..(1418)
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				175					180					185		
acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	629
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	
			190					195					200			
gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	677
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	
		205					210					215				
aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	725
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	
	220					225					230					
ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	773
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	
235					240					245					250	
gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	821
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	
			255					260						265		
gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	869
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	
			270					275					280			
gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	917
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	
	285					290						295				
ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	965
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	
	300					305					310					
aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	1013
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	
315					320					325					330	
tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	1061
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	
			335					340						345		
cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	1109
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	
			350					355					360			
gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	1157
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	
	365					370						375				
aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	1205
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	
	380					385					390					
atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	1253
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	
395					400					405					410	

acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	1301
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	
				415					420					425		
aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	1349
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	
			430					435					440			
tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	1397
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
		445					450					455				
ctc	tcc	ctg	tct	ccg	ggt	aaa										1418
Leu	Ser	Leu	Ser	Pro	Gly	Lys										
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<211> 465

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic sequence

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			20					25					30			
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	50					55					60					
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Gly	
65					70					75					80	
Glu	Asp	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Asp	Thr	Ser	Ala	Ser	
			85						90					95		
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
			100					105					110			
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Asn	Tyr	Val	Asp	Tyr	Trp	Gly	Gln	Gly	
		115					120					125				
Ser	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
	130						135				140					
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
145					150					155					160	
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
				165					170					175		

Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
			180					185					190		
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
			195				200					205			
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro
		210				215					220				
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys
225					230					235					240
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
				245					250					255	
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
			260					265					270		
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
		275					280					285			
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
		290				295					300				
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val
305					310					315					320
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
				325					330					335	
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
			340					345					350		
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
		355					360					365			
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
		370				375					380				
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
385					390					395					400
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
				405					410					415	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
			420					425					430		
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
		435					440					445			
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
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Lys															
465															

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<213> Artificial Sequence

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<221> CDS

<222> (24)..(1412)

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<223> Description of Artificial Sequence: Synthetic  
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gtg gca aca gct aca ggt gtc cac tcc cag gta cag cta gtg caa tca 101
Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser
                        15             20             25

ggg cct gaa gtg aag aag cct ggg gcc tca gtg aaa gtt tcc tgc aag 149
Gly Pro Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys
                        30             35             40

gct tct ggc tac acc ttc acc aac tat gga atg aac tgg gta agg cag 197
Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln
                        45             50             55

gcg cct gga cag ggg ctt gag tgg atg ggg tgg ata aac acc tac act 245
Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr
                        60             65             70

gga gag cca aca tat ggt gaa gat ttc aag gga cgg ttt gca ttc tct 293
Gly Glu Pro Thr Tyr Gly Glu Asp Phe Lys Gly Arg Phe Ala Phe Ser
                        75             80             85

cta gac aca tcc gcc agc aca gcc tat atg gag ctc agc tcg ctg aga 341
Leu Asp Thr Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg
                        95             100             105

tcc gag gac act gca gtc tat ttc tgt gcg aga ttt ggt aac tac gta 389
Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg Phe Gly Asn Tyr Val
                        110             115             120

gac tac tgg ggt caa gga tca cta gtc act gtc tcc tca gct tcc acc 437
Asp Tyr Trp Gly Gln Gly Ser Leu Val Thr Val Ser Ser Ala Ser Thr
                        125             130             135

aag ggc cca tcc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc 485
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
                        140             145             150

gag agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa 533
Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                        155             160             165             170

ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac 581
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                        175             180             185

acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc 629
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
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190										195					200					
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Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys					
		205						210					215							
aac	gta	gat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aga	gtt	gag	725				
Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu					
	220						225					230								
tcc	aaa	tat	ggg	ccc	cca	tgc	cca	ccg	tgc	cct	gca	cct	gag	ttc	gcg	773				
Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Ala					
235					240					245					250					
ggg	gca	cca	tca	gtc	ttc	ctg	ttc	ccc	cca	aaa	ccc	aag	gac	act	ctc	821				
Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu					
				255					260					265						
atg	atc	tcc	cgg	acc	cct	gag	gtc	acg	tgc	gtg	gtg	gtg	gac	gtg	agc	869				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser					
			270						275					280						
cag	gaa	gac	ccc	gag	gtc	cag	ttc	aac	tgg	tac	gtg	gat	ggc	gtg	gag	917				
Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu					
		285						290					295							
gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	ttc	aac	agc	acg	965				
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr					
	300						305					310								
tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	acc	1013				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Thr					
315						320				325					330					
ggc	aag	gcg	tac	aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	ccg	tcc	tcc	1061				
Gly	Lys	Ala	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser					
				335					340					345						
atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gag	cca	cag	1109				
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln					
			350					355					360							
gtg	tac	acc	ctg	ccc	cca	tcc	cag	gag	gag	atg	acc	aag	aac	cag	gtc	1157				
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val					
		365					370					375								
agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tac	ccc	agc	gac	atc	gcc	gtg	1205				
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val					
		380					385					390								
gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	1253				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro					
395						400				405					410					
ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	agg	cta	acc	1301				
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr					
				415					420					425						
gtg	gac	aag	agc	agg	tgg	cag	gag	ggg	aat	gtc	ttc	tca	tgc	tcc	gtg	1349				

Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val		
			430					435					440				
atg	cat	gag	gct	ctg	cac	aac	cac	tac	aca	cag	aag	agc	ctc	tgc	ctg		1397
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Cys	Leu		
		445					450					455					
tct	ctg	ggt	aaa	tga	gaattc												1418
Ser	Leu	Gly	Lys														
		460															

<210> 7  
 <211> 462  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 sequence

<400> 7

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly		
1				5					10					15			
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Val	Lys	Lys		
			20					25					30				
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe		
		35					40					45					
Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu		
	50					55					60						
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Gly		
	65				70					75					80		
Glu	Asp	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Asp	Thr	Ser	Ala	Ser		
				85					90					95			
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val		
			100					105					110				
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Asn	Tyr	Val	Asp	Tyr	Trp	Gly	Gln	Gly		
		115					120					125					
Ser	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe		
	130						135				140						
Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu		
	145				150					155					160		
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp		
				165					170					175			
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu		
			180					185					190				
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser		
		195					200						205				

Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	
210						215					220					
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	
225					230					235					240	
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Ala	Gly	Ala	Pro	Ser	Val	Phe	
				245					250					255		
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	
				260				265					270			
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	
		275					280					285				
Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	
	290					295					300					
Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	
305					310					315					320	
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Thr	Gly	Lys	Ala	Tyr	Lys	Cys	
				325					330					335		
Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	
			340					345					350			
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	
		355					360					365				
Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	
	370					375					380					
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	
385					390					395					400	
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
				405					410					415		
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	
			420					425					430			
Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	
		435					440					445				
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Cys	Leu	Ser	Leu	Gly	Lys			
	450					455					460					

<210> 8  
 <211> 1392  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (58)..(1386)

<220>  
 <223> Description of Artificial Sequence: Synthetic

sequence

<400> 8

atggattggc tgtggaactt gctattcctg atggcagctg cccaaagtat ccaagca	57
cag atc cag ttg gtg cag tct gga cct gaa ctg aag aag cct gga gag Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu 1 5 10 15	105
aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc aca aac tat Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr 20 25 30	153
gga atg aac tgg gtg agg cag gct tca gga gag ggt tta aag tgg atg Gly Met Asn Trp Val Arg Gln Ala Ser Gly Glu Gly Leu Lys Trp Met 35 40 45	201
ggc tgg ata aac acc tac act gga gag cca aca tat ggt gaa gat ttc Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Gly Glu Asp Phe 50 55 60	249
aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc tat Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr 65 70 75 80	297
ttg cag atc aac aac ctc aaa aat gaa gac acg gct aca tat ttc tgt Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys 85 90 95	345
gca aga ttt ggt aac tac gta gac tac tgg ggc caa ggc acc act ctc Ala Arg Phe Gly Asn Tyr Val Asp Tyr Trp Gly Gln Gly Thr Thr Leu 100 105 110	393
aca gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gcg Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala 115 120 125	441
ccc tgc tcc agg agc acc tcc gag agc aca gcg gcc ctg ggc tgc ctg Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu 130 135 140	489
gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly 145 150 155 160	537
gct ctg acc agc ggc gtg cac acc ttc cca gct gtc cta cag tcc tca Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser 165 170 175	585
gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc aac ttc Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe 180 185 190	633
ggc acc cag acc tac acc tgc aac gta gat cac aag ccc agc aac acc Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr 195 200 205	681
aag gtg gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro 729	

210	215	220	
tgc cca gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca			777
Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro			
225	230	235	240
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc			825
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys			
	245	250	255
gtg gtg gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg			873
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp			
	260	265	270
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag			921
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu			
	275	280	285
gag cag ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg			969
Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val			
	290	295	300
cac cag gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac			1017
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn			
	305	310	320
aaa ggc ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg			1065
Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly			
	325	330	335
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag			1113
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu			
	340	345	350
atg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac			1161
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr			
	355	360	365
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac			1209
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn			
	370	375	380
aac tac aag acc aca cct ccc atg ctg gac tcc gag ggc tcc ttc ttc			1257
Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe			
	385	390	400
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac			1305
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn			
	405	410	415
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac aca			1353
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr			
	420	425	430
cag aag agc ctc tgc ctg tct ctg ggt aaa tga gaattc			1392
Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys			
	435	440	

<211> 442  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
sequence

<400> 9

Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu	
1				5					10					15		
Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Ser	Gly	Glu	Gly	Leu	Lys	Trp	Met	
		35					40					45				
Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Gly	Glu	Asp	Phe	
	50					55					60					
Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	
	65				70					75					80	
Leu	Gln	Ile	Asn	Asn	Leu	Lys	Asn	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
				85					90					95		
Ala	Arg	Phe	Gly	Asn	Tyr	Val	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Leu	
			100					105					110			
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	
		115					120					125				
Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	
	130					135					140					
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	
	145				150					155					160	
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	
				165					170					175		
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Asn	Phe	
			180					185					190			
Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	
		195					200					205				
Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	
	210					215					220					
Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
	225				230					235					240	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
				245					250					255		
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	
			260					265					270			
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	

275						280						285					
Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val		
290						295			300								
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn		
305				310		315						320					
Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly		
			325			330						335					
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu		
			340			345						350					
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
355						360			365								
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
370						375			380								
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe		
385				390				395						400			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
			405			410						415					
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr		
			420			425						430					
Gln	Lys	Ser	Leu	Cys	Leu	Ser	Leu	Gly	Lys								
435						440											

<210> 10

<211> 1392

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
sequence

<400> 10

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gaattctcat ttaccacagag acaggcagag gctcttctgt gtgtagtggt tgtgcagagc 60
ctcatgcatc acggagcatg agaagacgtt cccctgctgc cacctgctct tgtccacggc 120
gagcttgctg tagaggaaga aggagccgtc ggagtccagc atgggaggtg tgggtcttgta 180
gttgttctcc ggctgccccat tgctctccca ctccacggcg atgtcgtctg ggtagaagcc 240
tttgaccagg caggtcaggc tgacctggtt cttgggtcatc tcctcccggg atgggggcag 300
gggtgtacacc tgtggttctc ggggctgccc tttggttttg gagatggttt tctcgatggg 360
ggctggggagg cctttgttgg agaccttgca cttgtactcc ttgccgttca gccagtcctg 420
gtgcacaacg gtgaggacgc tgaccacacg gaacgtgctg ttgaactgct cctcccgtgg 480
ctttgtcttg gcattatgca cctccacgcc gtccacgtac cagttgaact ggacctcggg 540
gtcttcgtgg ctacgtcca ccaccacgca cgtgacctca ggggtccggg agatcatgag 600
gggtgccttg ggttttgggg ggaagaggaa gactgacggt cctgccacag gtggtgctgg 660
gcacggtggg cactcgacac aacatttgcg ctcaactgtc ttgtccacct tgggtgttgct 720
gggcttgtag tctacgttgc aggtgtaggt ctgggtgccg aagttgctgg agggcacggc 780
caccacgctg ctgagggagt agagtcctga ggactgtagg acagctggga aggtgtgcac 840
gccgctgggc agagcgctg agttccacga caccgtcacc ggttcgggga agtagtcctt 900
gaccaggcag cccagggccg ctgtgctctc ggaggtgctc ctggagcagg gcgccagggg 960
gaagaccgat gggcccttgg tggaggctga ggagactgtg agagtgggtg cttggcccca 1020

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gtagtctacg tagttaccaa atcttgcaca gaaatatgta gccgtgtctt catttttgag 1080
gttggtgata tgcaaatagg cagtgtctggc agagggttcc aaagagaagg caaacccgtcc 1140
cttgaaatct tcaccatatg ttggctctcc agtgtagggtg tttatccagc ccatccactt 1200
taaaccctct cctgaagcct gcctcaccca gttcattcca tagtttgtga aggtatatcc 1260
agaagccttg caggagatct tgactgtctc tccagggttc ttcagttcag gtccagactg 1320
caccaactgg atctgtgctt ggatactttg ggcagctgcc atcaggaata gcaagttcca 1380
cagccaatcc at 1392

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<210> 11
<211> 238
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
sequence

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<400> 11
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1           5           10           15
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
          20           25           30
Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn Leu
          35           40           45
Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro
          50           55           60
Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser
          65           70           75           80
Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr
          85           90           95
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
          100          105          110
Ala Gln Asn Leu Glu Ile Pro Arg Thr Phe Gly Gln Gly Thr Lys Val
          115          120          125
Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
          130          135          140
Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
          145          150          155          160
Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
          165          170          175
Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
          180          185          190
Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
          195          200          205
Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly

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210		215		220
Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys				
225		230		235

<210> 12  
 <211> 465  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 sequence

<400> 12  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys  
 20 25 30  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 50 55 60  
 Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Gly  
 65 70 75 80  
 Glu Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Ala Ser  
 85 90 95  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Phe Cys Ala Arg Phe Gly Asn Tyr Val Asp Tyr Trp Gly Gln Gly  
 115 120 125  
 Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
 130 135 140  
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
 145 150 155 160  
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
 165 170 175  
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
 180 185 190  
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
 195 200 205  
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
 210 215 220  
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys  
 225 230 235 240

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
 245 250 255  
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
 260 265 270  
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
 275 280 285  
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
 290 295 300  
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
 305 310 315 320  
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 325 330 335  
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 340 345 350  
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
 355 360 365  
 Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr  
 370 375 380  
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
 385 390 395 400  
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
 405 410 415  
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
 420 425 430  
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
 435 440 445  
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
 450 455 460  
 Lys  
 465

<210> 13

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic sequence

<400> 13

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15



35					40					45					
Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
	50					55					60				
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Gly	Glu	Pro	Thr	Tyr	Gly
65					70					75					80
Glu	Asp	Phe	Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Asp	Thr	Ser	Ala	Ser
				85					90					95	
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105					110		
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Asn	Tyr	Val	Asp	Tyr	Trp	Gly	Gln	Gly
		115					120					125			
Ser	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
	130						135				140				
Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu
145					150					155					160
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
				165					170					175	
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
			180					185					190		
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
			195				200					205			
Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
	210					215					220				
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro
225					230					235				240	
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Ala	Gly	Ala	Pro	Ser	Val	Phe
				245					250					255	
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
			260					265					270		
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val
		275					280					285			
Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
						295					300				
Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
305					310					315					320
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Ala	Tyr	Lys	Cys
				325					330					335	
Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser
			340					345					350		
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
		355					360					365			

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 370 375 380  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 385 390 395 400  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 405 410 415  
 Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp  
 420 425 430  
 Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 435 440 445  
 Asn His Tyr Thr Gln Lys Ser Leu Cys Leu Ser Leu Gly Lys  
 450 455 460

<210> 15  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 sequence

<400> 15  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15  
 Val His Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val  
 20 25 30  
 Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn Leu  
 35 40 45  
 Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro  
 50 55 60  
 Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser  
 65 70 75 80  
 Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr  
 85 90 95  
 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys  
 100 105 110  
 Ala Gln Asn Leu Glu Ile Pro Arg Thr Phe Gly Gln Gly Thr Lys Val  
 115 120 125  
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
 130 135 140  
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
 145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 165 170 175  
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
 180 185 190  
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
 195 200 205  
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
 210 215 220  
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 225 230 235

<210> 16  
 <211> 461  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 sequence

<400> 16  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys  
 20 25 30  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 50 55 60  
 Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Gly  
 65 70 75 80  
 Glu Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Ala Ser  
 85 90 95  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110  
 Tyr Phe Cys Ala Arg Phe Gly Asn Tyr Val Asp Tyr Trp Gly Gln Gly  
 115 120 125  
 Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
 130 135 140  
 Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu  
 145 150 155 160  
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
 165 170 175  
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

180						185						190					
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser		
		195					200					205					
Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro		
	210					215					220						
Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu		
225					230					235					240		
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu		
				245					250					255			
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu		
			260					265					270				
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln		
		275					280					285					
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys		
	290					295					300						
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu		
305					310					315					320		
Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys		
				325					330					335			
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys		
			340					345					350				
Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser		
		355					360					365					
Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys		
	370					375					380						
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln		
385					390					395				400			
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly		
				405					410					415			
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln		
			420					425					430				
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn		
		435					440					445					
His	Tyr	Thr	Gln	Lys	Ser	Leu	Cys	Leu	Ser	Leu	Gly	Lys					
	450					455					460						